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Om protein - protein search, using sw model	(c) 1993 - 2003 Compugen Ltd.									
Run on:	April 8, 2003, 14:33:07 ; search time 47 seconds									
Scoring table:	OLIGO (without alignments)									
Word size :	8									
Total number of hits satisfying chosen parameters:	191									
Minimum DB seq length:	0									
Maximum DB seq length:	2000000000									
Post-processing: Listing first 1000 summaries										
Database :	PIR-73;*									
1: pir1;*										
2: pir2;*										
3: pir3;*										
4: pir4;*										
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
Result No.	Score	Query Match Length	DB ID	Description						
1	7.0	12.8	540 2	G95522 chaperonin, 60 kDa chaperonin GroEL [30	24	4.4	544 2	JL0117	
2	7.0	12.8	540 2	chaperonin GroEL [31	24	4.4	544 2	B1479	
3	5.6	10.3	542 2	B86574 60 kDa chaperonin [32	24	4.4	544 2	F86507	
4	3.1	5.7	542 2	AD1333 class I heat-shock heat shock protein	33	24	4.4	544 2	B81556	
5	2.7	5.0	542 2	S23918 T35591 heat shock protein	34	24	4.4	544 2	D88709	
6	2.7	5.0	544 2	B97442 GroEL protein - Ag	35	24	4.4	544 2	A62263	
7	2.7	5.0	544 2	60K chaperonin (pr	36	24	4.4	545 2	G81328	
8	2.7	5.0	544 2	AD2660 KDA chaperonin	37	24	4.4	546 2	I10342	
9	2.7	5.0	545 2	JN0309 heat shock protein	38	24	4.4	546 2	S23347	
10	2.7	5.0	545 2	S45310 chaperonin GroEL -	39	23	4.2	543 2	B41872	
11	2.7	5.0	545 2	C95311 chaperonin GroEL -	40	23	4.2	543 2	F97232	
12	2.7	5.0	547 2	I140311 chaperonin GroEL protein	41	23	4.2	544 2	S70667	
13	2.6	4.8	538 2	C89952 chaperonin GroEL [imp	42	23	4.2	545 2	S21563	
14	2.6	4.8	539 2	JN0601 heat shock protein	43	23	4.2	546 2	B43827	
15	2.6	4.8	541 2	JN0312 heat shock protein	44	23	4.2	546 2	A63640	
16	2.6	4.8	542 2	F93967 B84539 heat shock protein	45	23	4.2	547 2	JC2564	
17	2.6	4.8	542 2	AC1704 chaperonin GroEL -	46	23	4.2	547 2	B87353	
18	2.5	4.6	539 2	B49855 heat shock protein	47	22	4.0	544 1	B83094	
19	2.5	4.6	541 2	S68349 chaperonin GroEL h	48	22	4.0	544 1	A63827	
20	2.5	4.6	542 2	JN0661 heat shock protein	49	22	4.0	545 2	B43827	
21	2.5	4.6	542 2	S32106 heat shock protein	50	22	4.0	545 2	A63640	
22	2.5	4.6	544 2	JC5130 heat shock protein	51	21	3.9	545 2	S49253	
23	2.5	4.6	544 2	JC6063 heat shock protein	52	21	3.9	545 2	B44225	
24	2.5	4.6	544 2	B83702 heat shock protein	53	21	3.9	545 2	S39765	
25	2.4	4.4	538 2	J01195 heat shock protein	54	20	3.7	544 2	A26950	
26	2.4	4.4	544 2	A71555 probable esp-60 -	55	20	3.7	544 2	B43509	
27	2.4	4.4	544 2	B41884 58K heat shock protein	56	20	3.7	544 2	S40245	
28	2.4	4.4	544 2	S19023 heat shock protein	57	20	3.7	544 2	F44725	
29	2.4	4.4	544 2	I40731 heat shock protein	58	20	3.7	544 2	T06829	
30	2.4	4.4	544 2	S37039 heat shock protein	59	20	3.7	544 2	S56595	
31	2.4	4.4	544 2	A25902 heat shock protein	60	20	3.7	544 2	A26950	
32	2.4	4.4	544 2	JN0511 heat shock protein	61	19	3.5	541 2	S72614	
33	2.4	4.4	544 2	F70737 heat shock protein	62	19	3.5	541 2	B4VCGL	
34	2.4	4.4	544 2	H95269 heat shock protein	63	19	3.5	544 2	F82783	
35	2.4	4.4	544 2	S34993 heat shock protein	64	19	3.5	544 2	S22342	
36	2.4	4.4	544 2	S23342 heat shock protein	65	19	3.5	546 2	S35309	
37	2.4	4.4	544 2	F53111 heat shock protein	66	19	3.5	546 2	S35309	
38	2.4	4.4	544 2	F70737 heat shock protein	67	17	3.1	544 2	F70737	
39	2.4	4.4	544 2	H95269 heat shock protein	68	17	3.1	544 2	H95269	
40	2.4	4.4	544 2	F82783 heat shock protein	69	17	3.1	547 2	S22342	
41	2.4	4.4	544 2	S37566 heat shock protein	70	16	2.9	540 2	S37566	
42	2.4	4.4	544 2	C41325 heat shock protein	71	16	2.9	540 2	S37566	
43	2.4	4.4	544 2	B41325 heat shock protein	72	16	2.9	540 2	S37566	
44	2.4	4.4	544 2	S561304 heat shock protein	73	16	2.9	540 2	S37566	
45	2.4	4.4	544 2	T35591 heat shock protein	74	16	2.9	541 2	S561304	
46	2.4	4.4	544 2	D642438 heat shock protein	75	16	2.9	541 2	T35591	
47	2.4	4.4	544 2	S61302 heat shock protein	76	16	2.9	543 2	D642438	
48	2.4	4.4	544 2	S611304 heat shock protein	77	16	2.9	543 2	S61302	
49	2.4	4.4	544 2	S611304 heat shock protein	78	16	2.9	544 2	S61302	
50	2.4	4.4	544 2	S611304 heat shock protein	79	16	2.9	544 2	S611304	
51	2.4	4.4	544 2	H81166A heat shock protein	80	16	2.9	544 2	S611304	
52	2.4	4.4	544 2	H81166A heat shock protein	81	16	2.9	544 2	H81166A	
53	2.4	4.4	544 2	C81021A heat shock protein	82	16	2.9	544 2	H81166A	
54	2.4	4.4	544 2	D82412 heat shock protein	83	15	2.8	534 2	C81021A	
55	2.4	4.4	544 2	S26872 heat shock protein	84	15	2.8	534 2	D82412	
56	2.4	4.4	544 2	JC57711 heat shock protein	85	15	2.8	543 2	S26872	
57	2.4	4.4	544 2	B88204B heat shock protein	86	15	2.8	543 2	JC57711	
58	2.4	4.4	544 2	H70180 heat shock protein	87	15	2.8	544 2	B88204B	
59	2.4	4.4	544 2	B84539 heat shock protein	88	15	2.8	544 2	H70180	
60	2.4	4.4	544 2	JC4188 heat shock protein	89	15	2.8	547 2	B84539	
61	2.4	4.4	544 2	B849203 heat shock protein	90	15	2.8	547 2	JC4188	
62	2.4	4.4	544 2	BVECGI heat shock protein	91	15	2.8	548 2	B849203	
63	2.4	4.4	544 2	C64076 heat shock protein	92	15	2.8	548 2	BVECGI	
64	2.4	4.4	544 2	S842811 heat shock protein	93	15	2.8	548 2	C64076	
65	2.4	4.4	544 2	D91269 heat shock protein	94	15	2.8	548 2	S842811	
66	2.4	4.4	544 2	B84932 heat shock protein	95	15	2.8	548 2	D91269	
67	2.4	4.4	544 2	B86110A heat shock protein	96	15	2.8	548 2	B84932	
68	2.4	4.4	544 2	60 kDa chaperonin GroEL protein [imp	97	15	2.8	548 2	B86110A	
69	2.4	4.4	544 2	heat shock protein GroEL protein [imp	98	15	2.8	548 2	60 kDa chaperonin	
70	2.4	4.4	544 2	heat shock protein GroEL protein [imp	99	15	2.8	550 2	heat shock protein	
71	2.4	4.4	544 2	heat shock protein GroEL protein [imp	100	15	2.8	550 2	heat shock protein	
72	2.4	4.4	544 2	heat shock protein GroEL protein [imp	101	15	2.8	550 2	heat shock protein	
73	2.4	4.4	544 2	heat shock protein GroEL protein [imp	102	15	2.8	550 2	heat shock protein	
74	2.4	4.4	544 2	heat shock protein GroEL protein [imp	103	15	2.8	550 2	heat shock protein	
75	2.4	4.4	544 2	heat shock protein GroEL protein [imp	104	15	2.8	550 2	heat shock protein	
76	2.4	4.4	544 2	heat shock protein GroEL protein [imp	105	15	2.8	550 2	heat shock protein	
77	2.4	4.4	544 2	heat shock protein GroEL protein [imp	106	15	2.8	550 2	heat shock protein	
78	2.4	4.4	544 2	heat shock protein GroEL protein [imp	107	15	2.8	550 2	heat shock protein	
79	2.4	4.4	544 2	heat shock protein GroEL protein [imp	108	15	2.8	550 2	heat shock protein	
80	2.4	4.4	544 2	heat shock protein GroEL protein [imp	109	15	2.8	550 2	heat shock protein	
81	2.4	4.4	544 2	heat shock protein GroEL protein [imp	110	15	2.8	550 2	heat shock protein	
82	2.4	4.4	544 2	heat shock protein GroEL protein [imp	111	15	2.8	550 2	heat shock protein	
83	2.4	4.4	544 2	heat shock protein GroEL protein [imp	112	15	2.8	550 2	heat shock protein	
84	2.4	4.4	544 2	heat shock protein GroEL protein [imp	113	15	2.8	550 2	heat shock protein	
85	2.4	4.4	544 2	heat shock protein GroEL protein [imp	114	15	2.8	550 2	heat shock protein	
86	2.4	4.4	544 2	heat shock protein GroEL protein [imp	115	15	2.8	550 2	heat shock protein	
87	2.4	4.4	544 2	heat shock protein GroEL protein [imp	116	15	2.8	550 2	heat shock protein	
88	2.4	4.4	544 2	heat shock protein GroEL protein [imp	117	15	2.8	550 2	heat shock protein	
89	2.4	4.4	544 2	heat shock protein GroEL protein [imp	118	15	2.8	550 2	heat shock protein	
90	2.4	4.4	544 2	heat shock protein GroEL protein [imp	119	15	2.8	550 2	heat shock protein	
91	2.4	4.4	544 2	heat shock protein GroEL protein [imp	120	15	2.8	550 2	heat shock protein	
92	2.4	4.4	544 2	heat shock protein GroEL protein [imp	121	15	2.8	550 2	heat shock protein	
93	2.4	4.4	544 2	heat shock protein GroEL protein [imp	122	15	2.8	550 2	heat shock protein	
94	2.4	4.4	544 2	heat shock protein GroEL protein [imp	123	15	2.8	550 2	heat shock protein	
95	2.4	4.4	544 2	heat shock protein GroEL protein [imp	124	15	2.8	550 2	heat shock protein	
96	2.4	4.4	544 2	heat shock protein GroEL protein [imp	125	15	2.8	550 2	heat shock protein	
97	2.4	4.4	544 2	heat shock protein GroEL protein [imp	126	15	2.8	550 2	heat shock protein	
98	2.4	4.4	544 2	heat shock protein GroEL protein [imp	127	15	2.8	550 2	heat shock protein	
99	2.4	4.4	544 2	heat shock protein GroEL protein [imp	128</td					

A; Residues: 1-540 <KUR>	Qy	242	NRPLIITADDVGDEALPVLINKIRGTFNTVAVAKAPGSGDRRKAMLEDIAILTGGTIVRE 301	Best Local Similarity 100.0%; Score 70; DB 2; Length 540; Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
C; Cross-references: GB:AE007317; PIDN:ALL00525.1; PID:915459401; GSPDB:GN00174	C; Genomic:	Db	242	NRPLIITADDVGDEALPVLINKIRGTFNTVAVAKAPGSGDRRKAMLEDIAILTGGTIVRE 301	Qy 302 DLGIELKDAT 311 Db 302 DLGIELKDAT 311	
A; Gene: groEL	C; Superfamily: chaperonin groEL	RESULT 3	B36917	heat shock protein GroEL - Agrobacterium tumefaciens	Qy 266 RGTFNVVAVKAPGFGDRRKAMLEDIAILTGG 296	
C; Species: Lactococcus lactis subsp. lactis (strain ITL1403)	C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001	C; Species: Agrobacterium tumefaciens	Db 266 RGTFNVVAVKAPGFGDRRKAMLEDIAILTGG 296			
C; Accession: B86674	R; Boilot, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, P.; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis B86625; MUID:21235186; PMID:11337471	C; Accession: B36917	R; Segal, G.; Ron, E.Z.; Bacteriol. 175, 3083-3088, 1993	A; Status: Preliminary	A; Accession: B36917; MUID:93259955; PMID:8098329	
A; Reference number: B86674	J. Bacteriol. 175, 3083-3088, 1993	A; Molecule type: DNA	A; Molecule type: DNA	A; Status: Preliminary	A; Accession: B36917	
A; Reference number: B86625; MUID:21235186; PMID:11337471	A; Status: Preliminary	A; Cross-references: GB:AE00516; PID:912723267; PIDN:AAK04492.1; GSPDB:GN00146	A; Residues: 1-544 <SEG>	A; Note: Sequence extracted from NCBI backbone (NCBIN:131959, NCBIPI:131961)	A; Accession: B36917	
A; Experimental source: strain ITL1403	C; Genetics:	C; Superfamily: chaperonin groEL	C; Superfamily: Chaperonin groEL	C; Superfamily: Chaperonin groEL	C; Superfamily: Chaperonin groEL	
A; Gene: groEL	Query Match 10.3%; Score 55; DB 2; Length 542; Best Local Similarity 100.0%; Pred. No. 5e-47; Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 44 GSPLINGGYIAKIELEDDHFENNGAKLVSEASKTNIDAGDTTTATVLTCAIV 99 Db 44 GSPLINGGYIAKIELEDDHFENNGAKLVSEASKTNIDAGDTTTATVLTCAIV 99	Query Match 5.0%; Score 27; DB 2; Length 544; Best Local Similarity 100.0%; Pred. No. 3.7e-18; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTIV 299 Db 275 AVKAPGFGDRRKAMLEDIAILTGGTIV 301	Query Match 5.0%; Score 27; DB 2; Length 544; Best Local Similarity 100.0%; Pred. No. 3.7e-18; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTIV 299 Db 275 AVKAPGFGDRRKAMLEDIAILTGGTIV 301	Query Match 5.0%; Score 27; DB 2; Length 544; Best Local Similarity 100.0%; Pred. No. 3.7e-18; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTIV 299 Db 275 AVKAPGFGDRRKAMLEDIAILTGGTIV 301	Query Match 5.0%; Score 27; DB 2; Length 544; Best Local Similarity 100.0%; Pred. No. 3.7e-18; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTIV 299 Db 275 AVKAPGFGDRRKAMLEDIAILTGGTIV 301	
RESULT 4	ADJ333	class I heat-shock protein (chaperonin) GroEL [imported] - Listeria monocytogenes (strain C; Species: Listeria monocytogenes C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C; Accession: ADJ333 R; Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bleeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.H.; Fsihi, H.; D.; Jones, L.M.; Kast, U.; Science 294, 849-852, 2001 A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madierno, E.; Maitournam, A.; Madoño, C.; Schlueter, T.; Simoes, N.; Terraz, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Title: Comparative genomics of Listeria species. A; Status: Preliminary A; Accession: ADJ333 A; Status: Preliminary A; Molecule type: DNA	S23918	groEL protein - Agrobacterium tumefaciens	C; Species: Agrobacterium tumefaciens	C; Accession: S23918 R; Segal, G.; Ron, E.Z.; Submitted to the EMBL data library, August 1992 A; Description: Cloning and sequencing of the GroE operon of Agrobacterium tumefaciens A; Accession: S23918 A; Status: Preliminary A; Molecule type: DNA
A; Cross-references: EMBL:X68263; NID:910913; PIDN:CAA48331.1; PID:939095	C; Superfamily: chaperonin groEL	Query Match 5.0%; Score 27; DB 2; Length 544; Best Local Similarity 100.0%; Pred. No. 3.7e-18; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTIV 299 Db 275 AVKAPGFGDRRKAMLEDIAILTGGTIV 301	Query Match 5.0%; Score 27; DB 2; Length 544; Best Local Similarity 100.0%; Pred. No. 3.7e-18; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTIV 299 Db 275 AVKAPGFGDRRKAMLEDIAILTGGTIV 301	Query Match 5.0%; Score 27; DB 2; Length 544; Best Local Similarity 100.0%; Pred. No. 3.7e-18; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTIV 299 Db 275 AVKAPGFGDRRKAMLEDIAILTGGTIV 301	Query Match 5.0%; Score 27; DB 2; Length 544; Best Local Similarity 100.0%; Pred. No. 3.7e-18; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTIV 299 Db 275 AVKAPGFGDRRKAMLEDIAILTGGTIV 301	
RESULT 5	B97442	60k chaperonin (protein cpn60) (groEL protein) [imported] - Agrobacterium tumefaciens	C; Species: Agrobacterium tumefaciens	C; Accession: B97442 R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; La Science 294, 2323-2328, 2001 A; Title: Genome sequence of the Plant Pathogen and Biotechnology 1 A; Reference number: ADJ359; PMID:1743194	Best Local Similarity 100.0%; Pred. No. 3.8e-22; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 266 RGTFNVVAVKAPGFGDRRKAMLEDIAILTGG 296 Db 266 RGTFNVVAVKAPGFGDRRKAMLEDIAILTGG 296	

Query Match 5.0%; Score 27; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFDRRKAMMEDIALILTGGVVI 299
 Db 275 AVKAPGFDRRKAMMEDIALILTGGVVI 301

RESULT 8

AD2660 KDa chaperonin [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
 C;Accession: AD2660
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romeo, P.; Zhang, S.
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Parry, M.; Gordon-Kamm, A.;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; PMID:11743193
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:AE008688; PIDN:AAL41698.1; PID:917739044; GSPDB:GN00186
 C;Genetics:
 A;Gene: groEL
 A;Map position: circular chromosome
 C;Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFDRRKAMMEDIALILTGGVVI 299
 Db 275 AVKAPGFDRRKAMMEDIALILTGGVVI 301

RESULT 9

JN0509 heat shock protein groEL (clone Rhiz A) - Rhizobium meliloti
 N;Alternate names: Chaperonin groEL protein
 C;Species: Rhizobium meliloti
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
 C;Accession: JN0509
 R;Rusanganwa, E.; Gupta, R.S.
 Gene 126, 67-75, 1993
 A;Title: Cloning and characterization of multiple groEL chaperonin-encoding genes in Rhi
 A;Reference number: JN0509; MUID:93331539; PMID:8097179
 A;Accession: JN0509
 A;Molecule type: DNA
 A;Residues: 1-345 <RUS>
 A;Cross-references: GB:MH4192; NID:9152233; PIDN:AA26285.1; PID:9152235
 C;Comment: This protein plays a role in protein folding and in the extracellular transpic
 A;Gene: groEL
 C;Superfamily: chaperonin groEL
 C;Keywords: heat shock; molecular chaperone; stress-induced protein
 Query Match 5.0%; Score 27; DB 2; Length 545;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFDRRKAMMEDIALILTGGVVI 299
 Db 275 AVKAPGFDRRKAMMEDIALILTGGVVI 301

RESULT 10

S4530 chaperonin groEL - Porphyromonas gingivalis
 C;Species: Porphyromonas gingivalis
 C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
 C;Accession: S4530
 R;Hotokozaka, H.; Hayashida, H.; Ohara, N.; Nomaguchi, H.; Kobayashi, K.; Yamada, T.
 B;Biolchim. Biophys. Acta 1219, 155-158, 1994
 A;Title: Cloning and sequencing of the groEL homologue from Porphyromonas gingivalis
 A;Reference number: S47530; MUID:9136881; PMID:8084660
 A;Accession: S47530
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-545 <HOT>
 A;Note: the source is designated as *Bacteroides gingivalis*
 C;Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 545;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFDRRKAMMEDIALILTGGVVI 299
 Db 275 AVKAPGFDRRKAMMEDIALILTGGVVI 301

RESULT 11

C95311 groEL2 chaperonin [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSym
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C;Accession: C95311
 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barlow-Hubler, F.;
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium mel*
 A;Reference number: A95262; MUID:21396509; PMID:1181432
 A;Accession: C95311
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-545 <KUR>
 A;Cross-references: GB:AE006469; PIDN:AK6053.1; PID:914523485; GSPDB:GN00165
 A;Experimental source: strain 1021 megaplasmid pSym
 R;Gallibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlow-Hubler, F.;
 Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Fedderspiel, N.A.; Fisher, R.;
 L.; Hyman, R.W.; Jones, T.; Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lela,
 Hebuilt, P.; Vandembroucq, M.; Vorholt, F.J.; Waldner, S.; Wells, D.H.; Wong, K.; Yeh,
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: groEL2
 A;Genome: plasmid
 C;Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 545;
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFDRRKAMMEDIALILTGGVVI 299
 Db 275 AVKAPGFDRRKAMMEDIALILTGGVVI 301

